

## FIGURE 1

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA  
CAAGAAGCCGCCGCCTGCCTGCCCCGGGCCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCATAAATGCTGTGTGGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGTGTTGT

## FIGURE 2

MRSGCVVHVHVLWILAGLWLA VAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCF LRI  
RADGVVDCARGQSAHSLLEIKAV ALRTVAIKGVH SVRYLCMGADGKMQGLLO YSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

signal peptide:  
amino acids 1-22

N-myristoylation sites:  
amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site:  
amino acids 48-59

HBGF/FGF domain:  
amino acids 80-131

FIGURE 3B

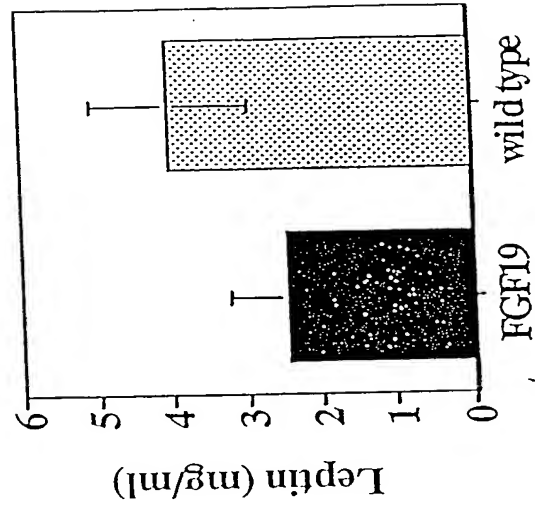


FIGURE 3A

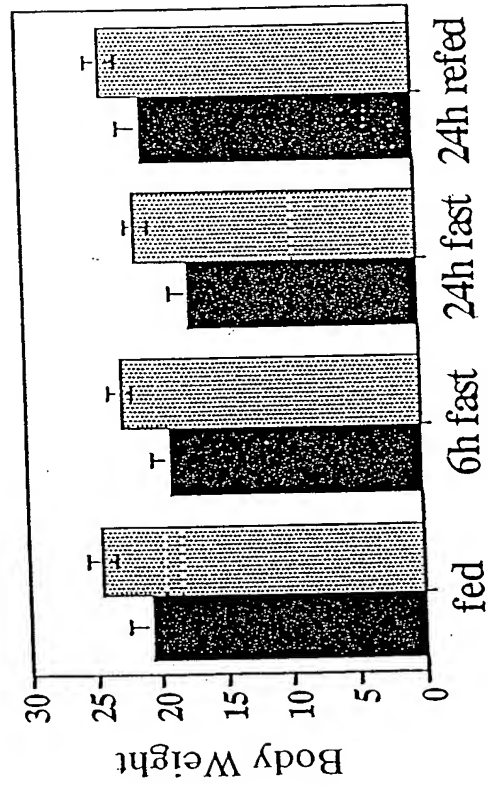


FIGURE 4B

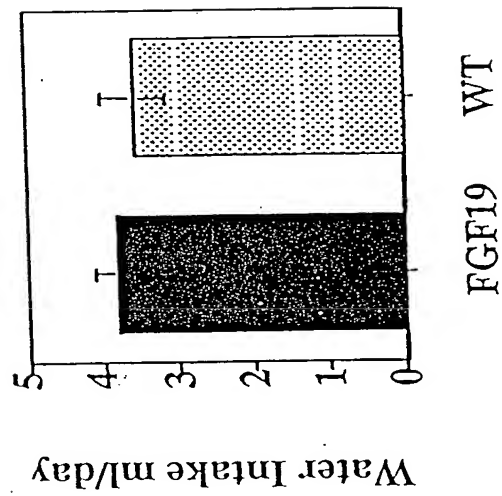


FIGURE 4A

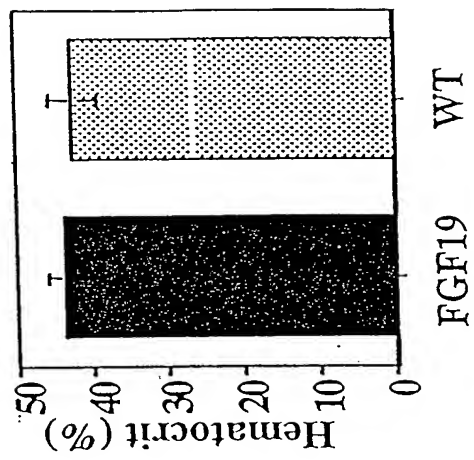
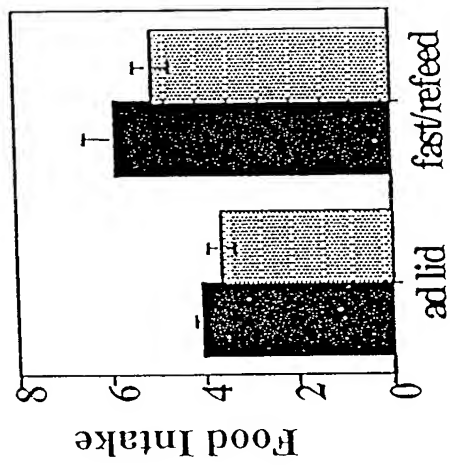


FIGURE 4D

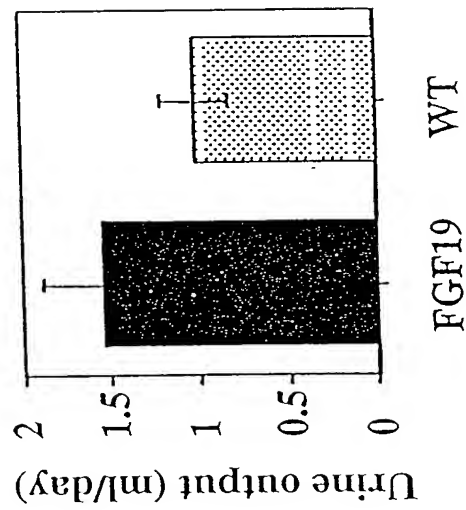


FIGURE 4C

FIGURE 5

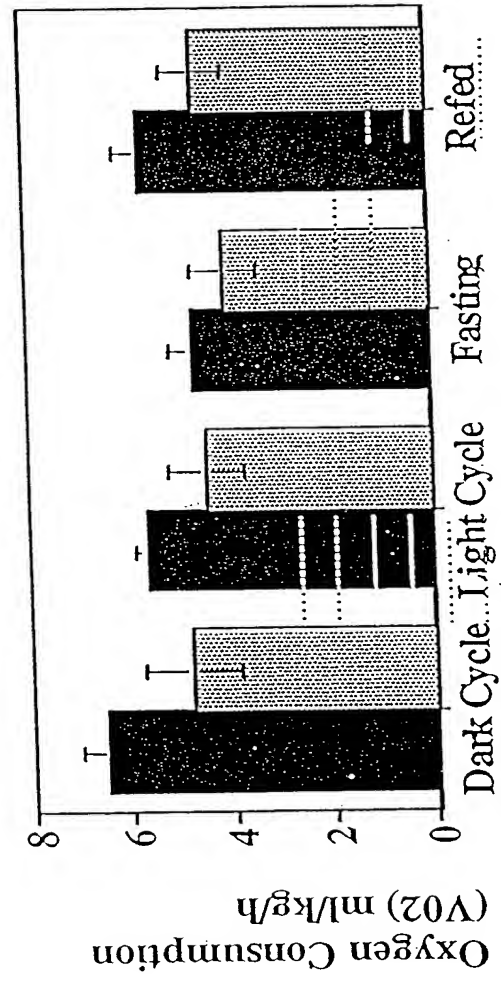


FIGURE 6B

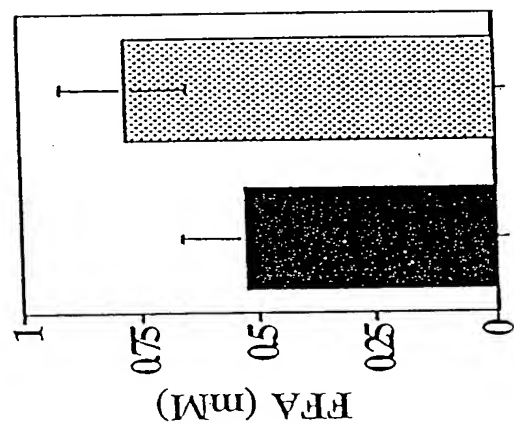


FIGURE 6A

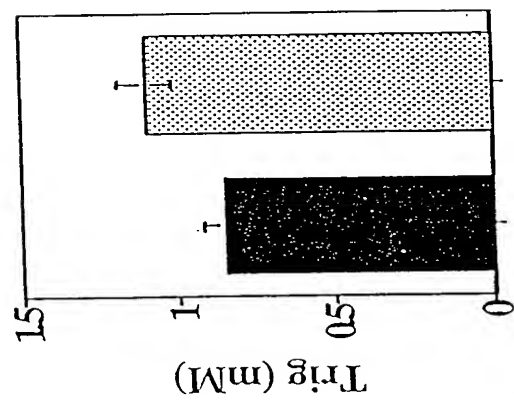


FIGURE 7B

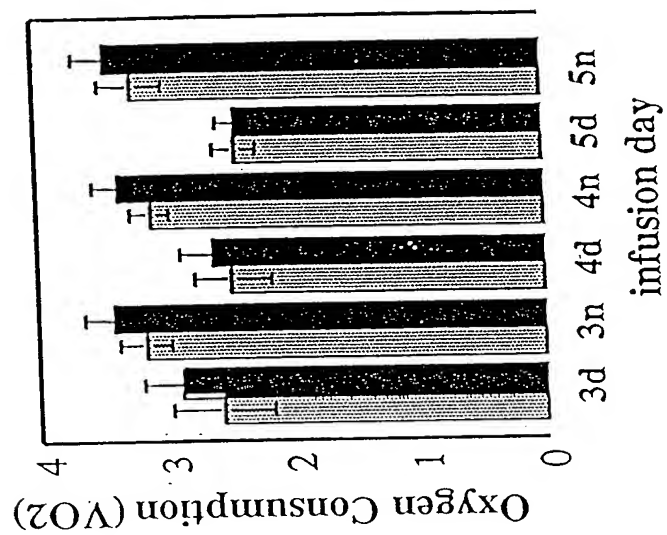


FIGURE 7A

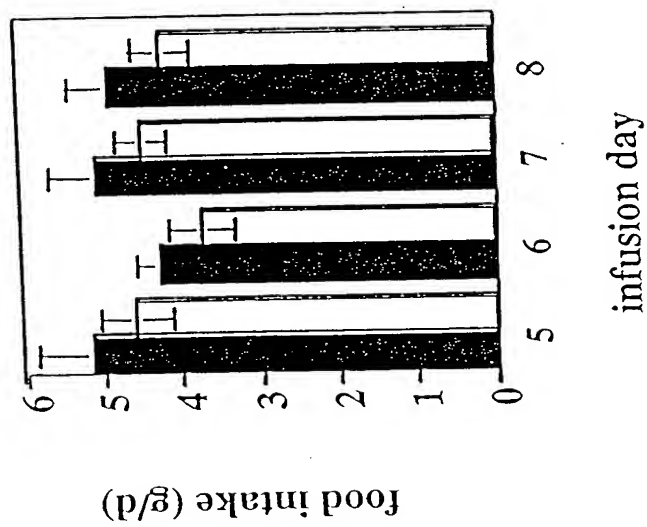


FIGURE 8B

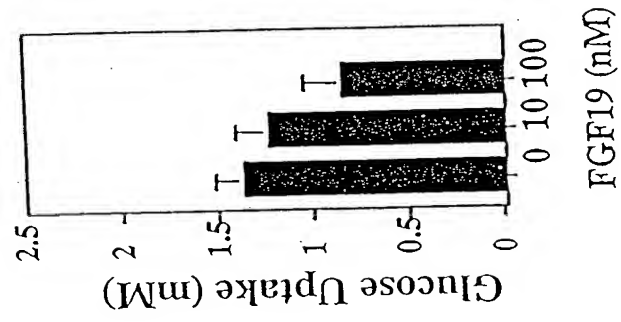
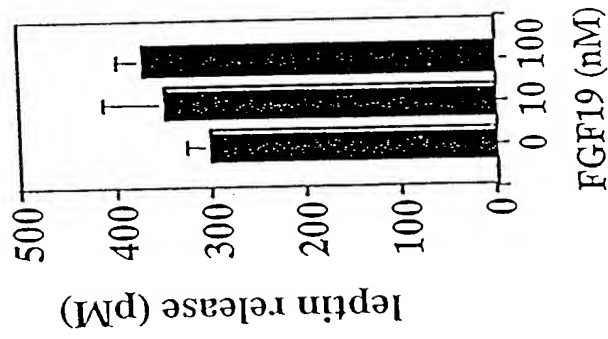


FIGURE 8A





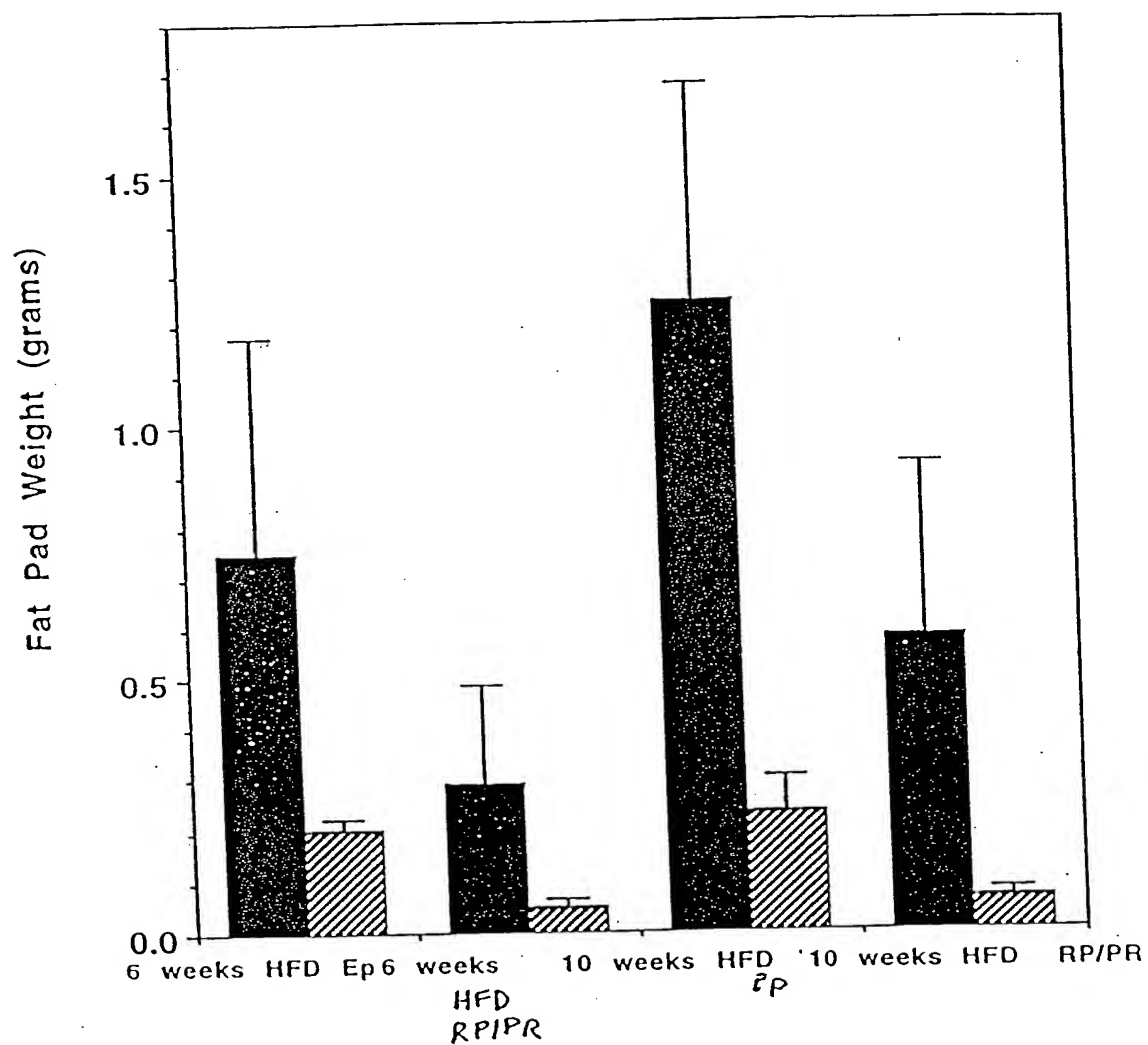


FIGURE 9

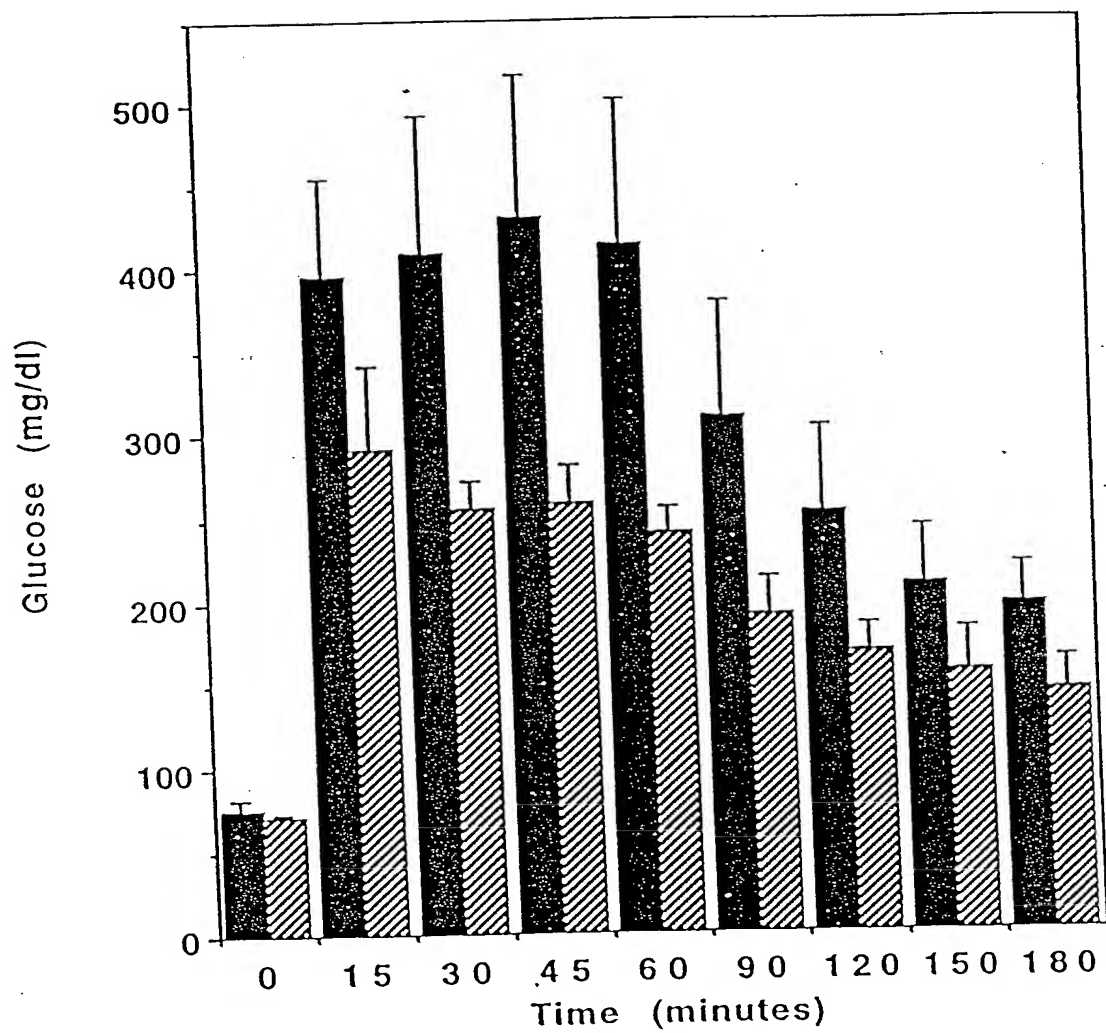


FIGURE 10

Fig. 11

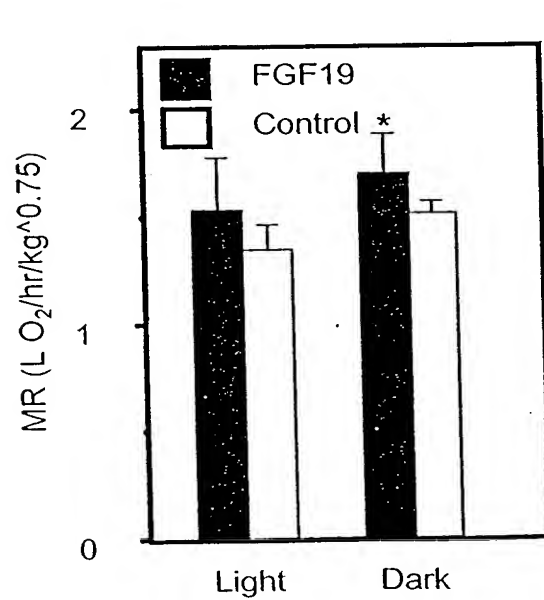
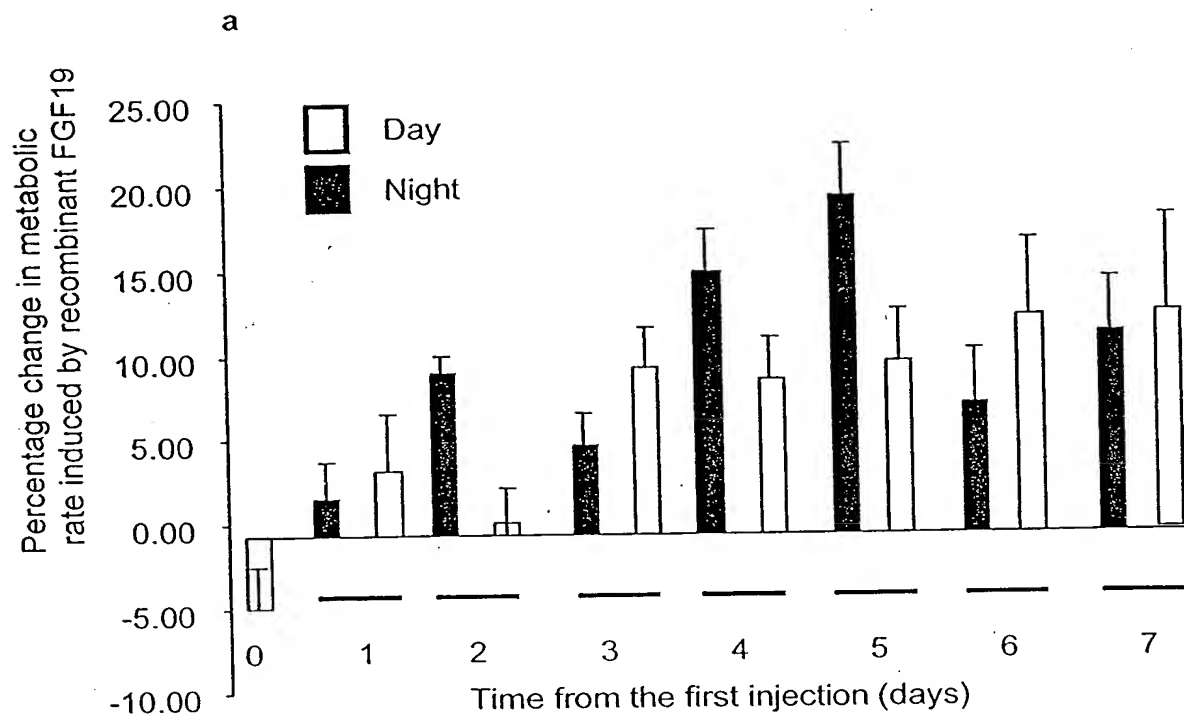


Fig 12

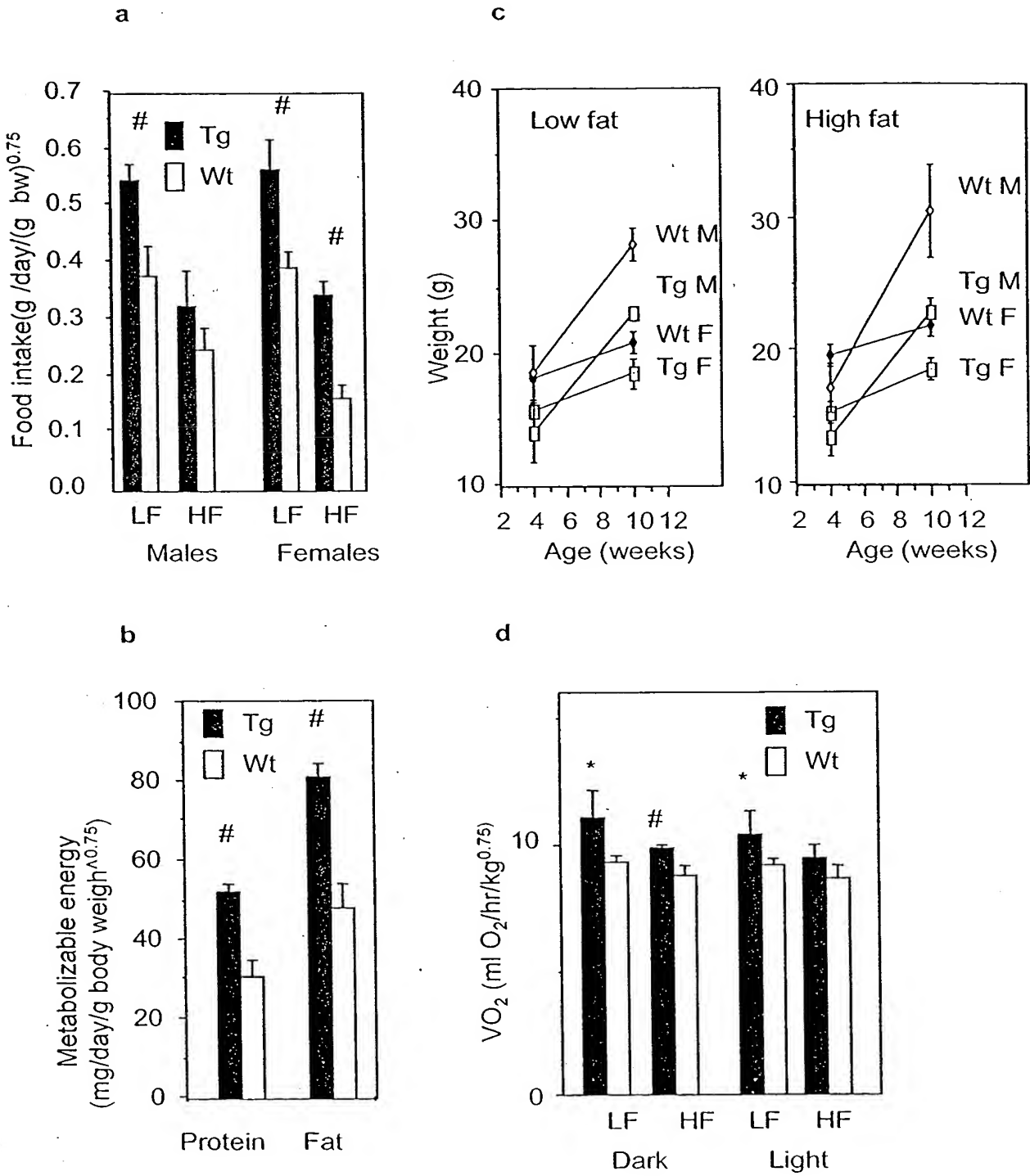


Fig. 13

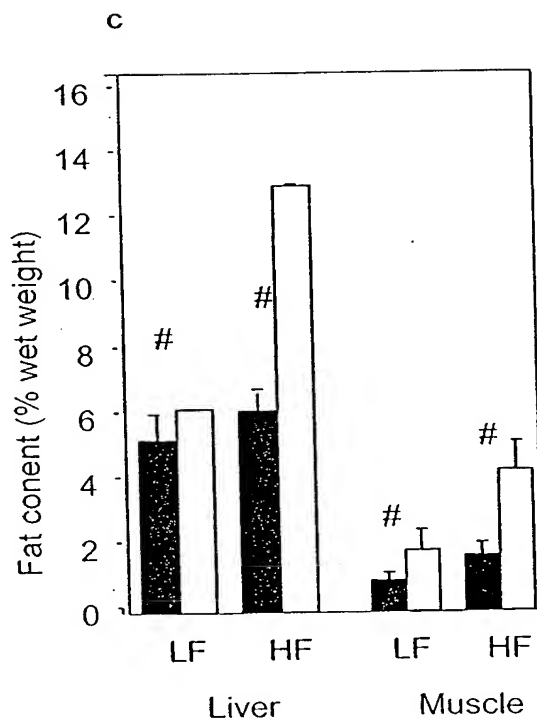
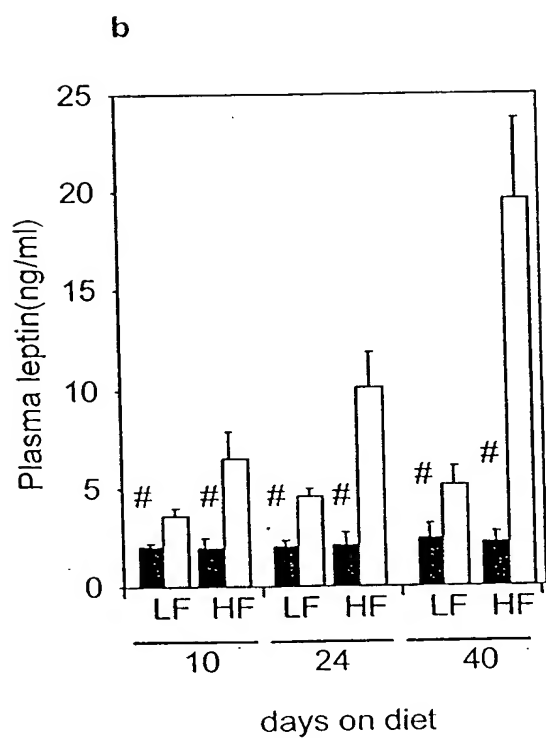
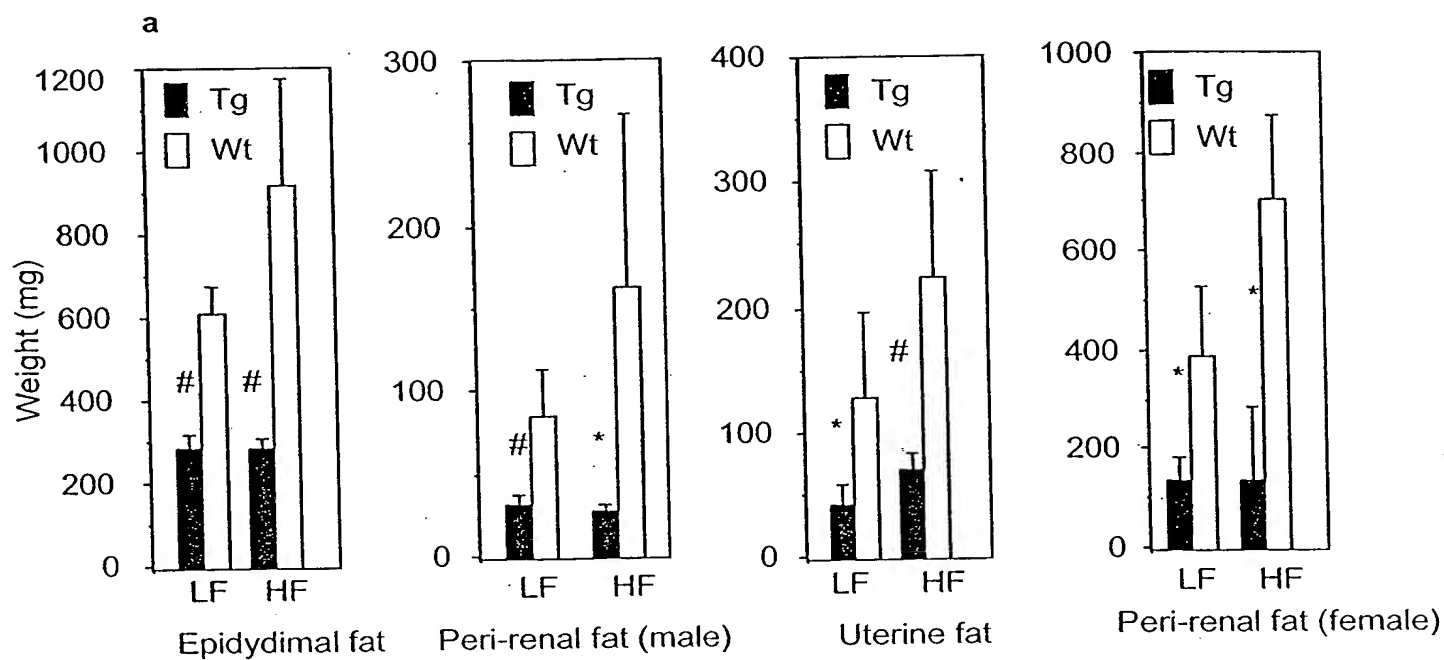


Fig. 14.

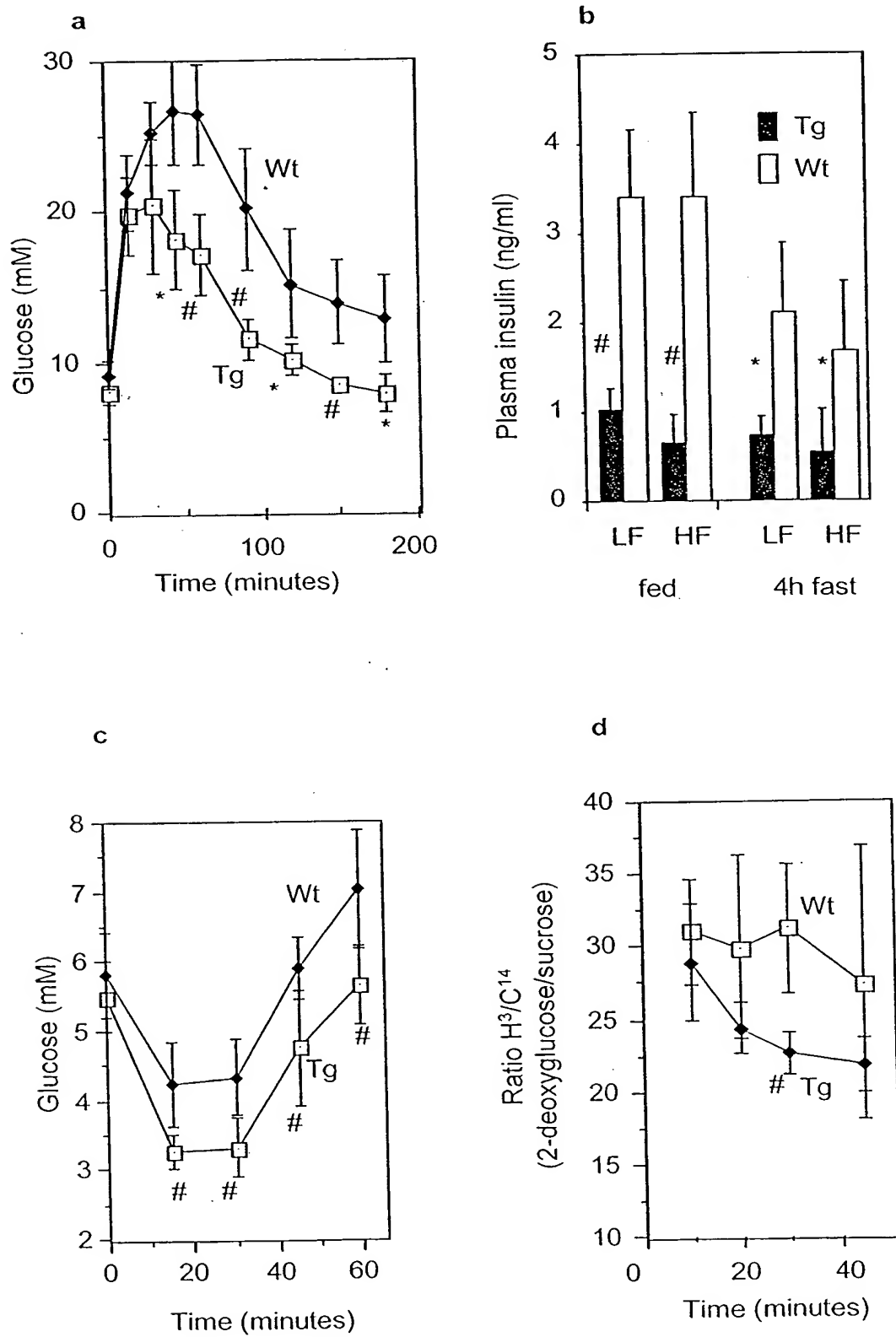


Fig. 15.

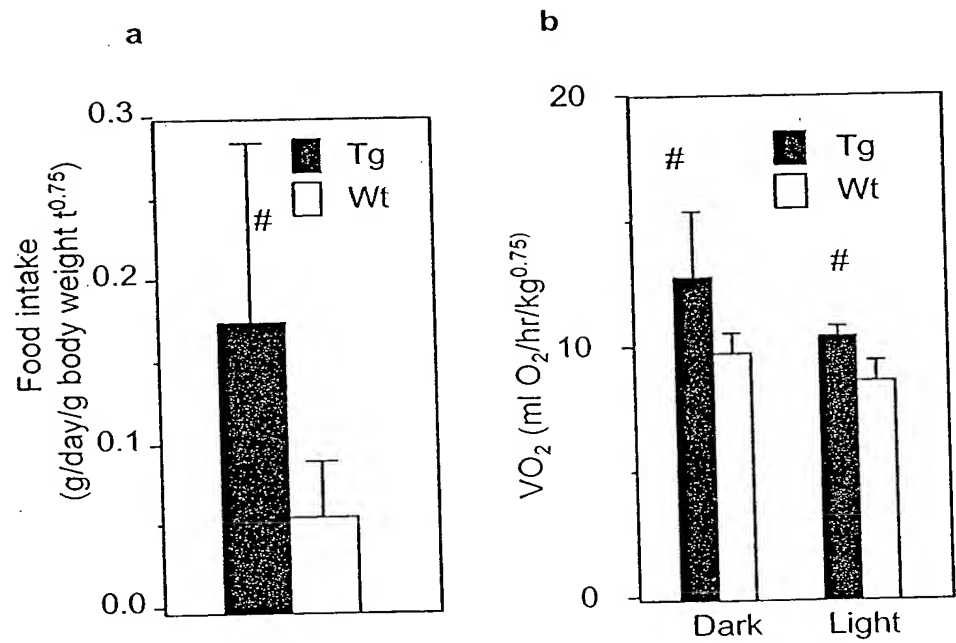
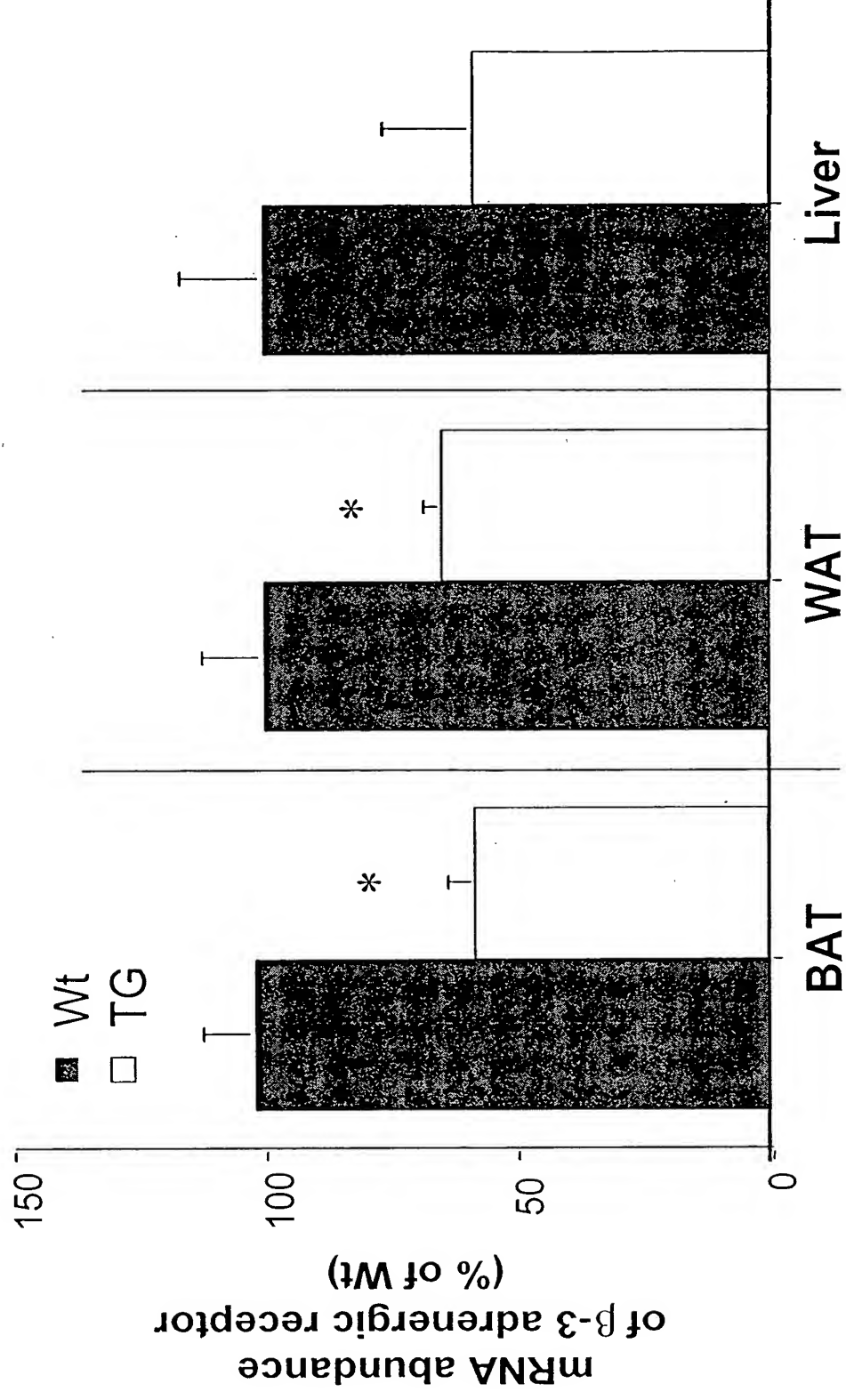


Figure 16



\*P < 0.05 vs Wt controls



# Figure 17

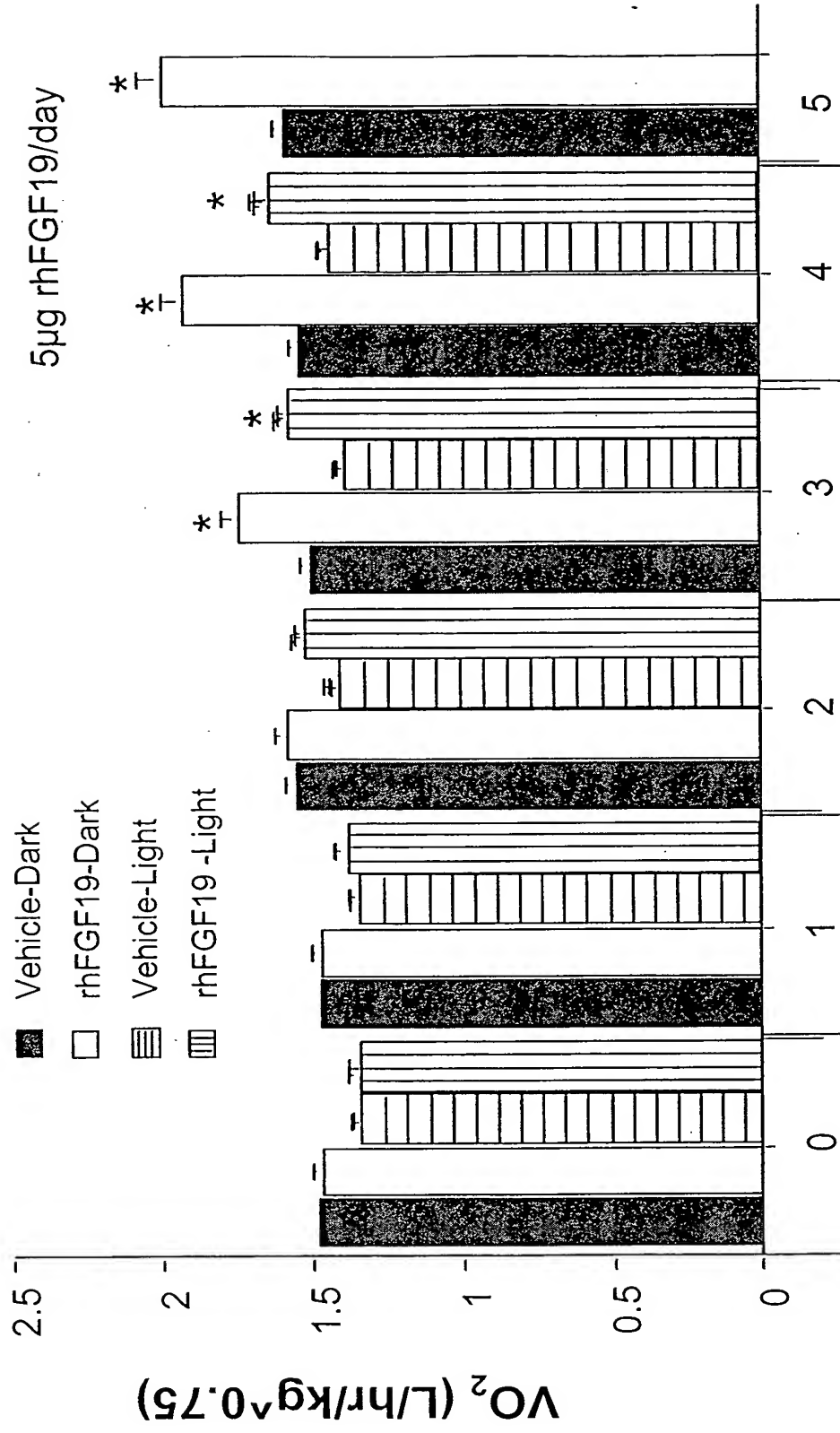


Figure 18

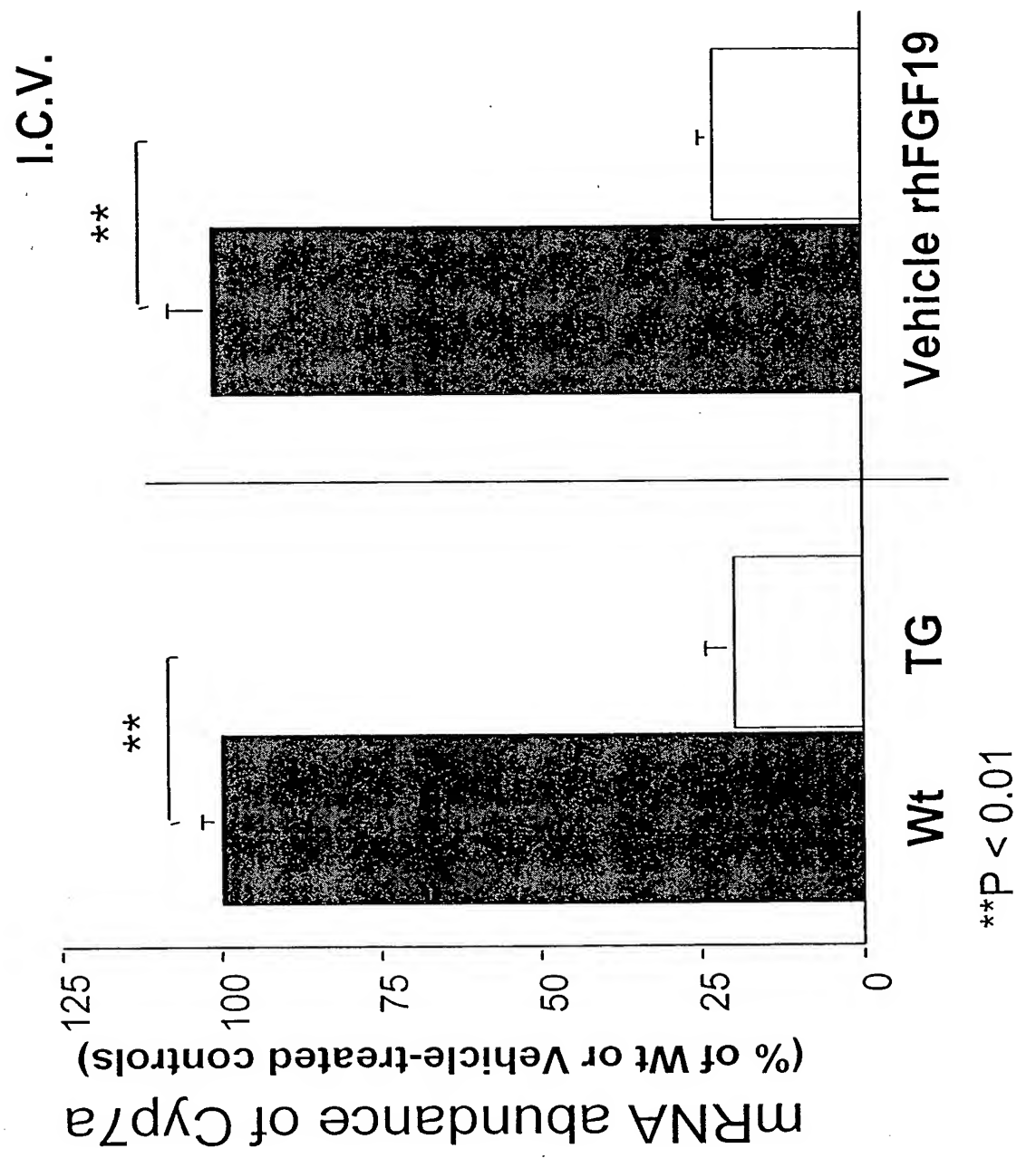


Figure 19

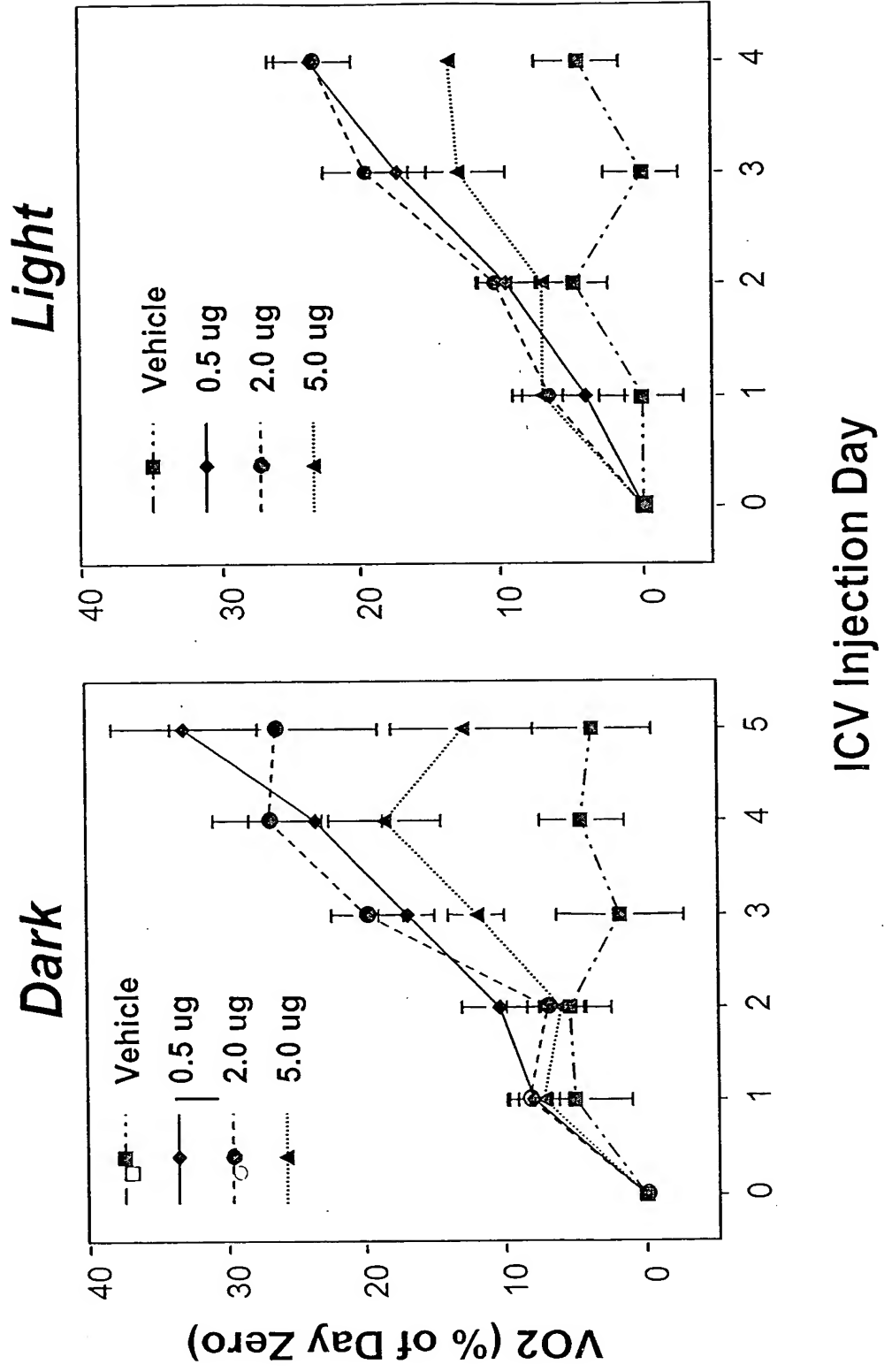


Figure 20

	rhFGF19			
	<u>Vehicle</u>	<u>5.0 µg</u>	<u>2.0 µg</u>	<u>0.5 µg</u>
NPY	1.0 +/- 0.08	0.81 +/- 0.23	0.63 +/-0.20	0.40 +/- 0.08
AgRP	1.0 +/- 0.33	0.26 +/- 0.10	0.57 +/- 0.26	0.29 +/- 0.16
POMC	1.0 +/- 0.27	1.49 +/- 0.42	3.48 +/- 1.5	38.77 +/- 3.32
MC4-R	1.0 +/- 0.16	0.47 +/- 0.09	0.70 +/- 0.10	0.48 +/- 0.08

